program is Gap which considers all possible alignment and gap positions and creates an alignment with the largest number of matched bases and the fewest gaps. Gap uses the alignment method of Needleman and Wunsch. Gap reads a scoring matrix that contains values for every possible GCG symbol match. GAP is available on the ANGIS (Australian National Genomic Information Service) website.

**Please replace the first paragraph on page 63 with the following amended paragraph:**

We next explored whether all isoforms of Bim were equivalent. An FDC-P1 clone expressing human Bcl-2 was transfected with vectors expressing $Bim_{EL}$, $Bim_{L}$ or $Bim_{S}$ and puromycin-resistant clones that expressed the same amount of each isoform were selected for further analysis (Figure 6A). To test for association with Bcl-2, immunoprecipitates prepared from cell lysates using a monoclonal antibody specific for human Bcl-2 were fractionated electrophoretically and blotted with anti-EE antibody. Each of the Bim isoforms clearly bound to Bcl-2 (Figure 6B). However, when the transfectants were deprived of IL-3 or subjected to γ-irradiation, it became evident that $Bim_{S}$ antagonised Bcl-2 more effectively than $Bim_{L}$ while $Bim_{EL}$ was the least potent (Figures 6C). In addition, $Bim_{S}$ suppressed L929 colony formation more effectively than $Bim_{L}$ or $Bim_{EL}$. Thus, although all three Bim isoforms can bind to Bcl-2, they vary in cytotoxicity, Bims being the most potent.

**In the claims**

Please cancel claims 1-5, 10-14, 23-27, 31-35, and 37-61 and substitute the following amended versions for claims 6-9, 15-22, 28, and 29. A marked-up version showing changes made is appended.

6. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence encoding or complementary to a sequence encoding an amino acid sequence of SEQ ID NO:10 or having at least about 45% or greater identity to SEQ ID NO:10 wherein said amino acid sequence is characterized by the ability to induce apoptosis.

7. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:9 or capable of hybridising to SEQ ID NO: 9 under moderate stringency conditions wherein said nucleic acid molecule encodes a polypeptide characterized by the ability to induce apoptosis.

D3 8. (Amended) An isolated nucleic acid molecule according to claim 7 which further encodes an amino acid sequence corresponding to an amino acid sequence of SEQ ID NO:10 or having at least about 45% or greater identity to SEQ ID NO:10.

9. (Amended) An isolated nucleic acid molecule according to claim 7 of SEQ ID NO:9.

15. (Amended) An isolated polypeptide comprising an amino acid sequence of SEQ ID NO:10 or a sequence having at least about 45% identity to SEQ ID NO:10, wherein said polypeptide is characterized by the ability to induce apoptosis.

D4 16. (Amended) An isolated polypeptide according to claim 15 encoded by a nucleotide sequence of SEQ ID NO:9 under moderate stringency conditions.

17. (Amended) An isolated polypeptide according to claim 16 further comprising an amino acid sequence of SEQ ID NO:10 or a sequence having at least about 45% identity to SEQ ID NO:10.

D5 18. (Twice Amended) An isolated polypeptide according to claim 16 having SEQ ID NO:10.

D6 19. (Twice Amended) An isolated polypeptide according to claim 15 in homodimeric form.

D7 20. (Twice Amended) An isolated polypeptide according to claim 15 in heterodimeric form.

D8 21. (Twice Amended) A variant of an isolated nucleic acid molecule as claimed in claim 6 comprising one or more nucleotide mutations in said nucleic acid molecule

resulting in at least one amino acid addition, substitution and/or deletion to the polypeptide encoded by said variant wherein said polypeptide cannot bind, couple or otherwise associate with a dynein light chain and wherein said polypeptide is characterized by the ability to induce apoptosis.

22. (Amended) A variant according to claim 21 wherein said mutation results in an amino acid addition, substitution and/or deletion in the region of the polypeptide chain which binds the dynein light chain.

28. (Amended) A variant according to claim 22 wherein said nucleic acid molecule is human *Bim*EL and said region is defined by amino acid residue numbers 42 to 131.

29. (Amended) A variant of an isolated polypeptide as claimed in claim 15 comprising at least one amino acid addition, substitution, and/or deletion wherein said variant cannot bind, couple or otherwise associate with the dynein light chain.